

Figure 1
Interleukin-21

1 GGCACGAGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCT 60
1 A R V D T D E D R Y P Q K L A F A E C L 20
Domain I Domain II

61 GTGCAGAGGCTGTATCGATGCACGGACGGGCGCGAGACAGCTGCGCTCAACTCCGTGCG 120
21 C R G C I D A R T G R E T A A L N S V R 40
Domain II

121 GCTGCTCCAGAGCCTGCTGGTGTGCGCCGCGGCCCTGCTCCCGCGACGGCTCGGGGCT 180
41 L L Q S L L V L R R R P C S R D G S G L 60
Domain III

181 CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCAGTCCCCGTCGGCTGCAC 240
61 P T P G A F A F H T E F I H V P V G C T 80
Domain IV

241 CTGCGTGTGCCCCGTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACACGT 300
81 C V L P R S V 87
Domain IV

301 GTGCTCCCCAGAGGGCACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCC 360

361 AACACTACCCCTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTC 420

421 CTCATCTCCAGCCTCAGTAGTGGGGGTWGAAGGAGCTCAGCACCTCTTCCAGCCCTTAA 480

481 AGCTGCAGAAAAGGTGTACACGGCTGCCTGTACCTTGGYTCCCTGTCTGCTCCCGGCT 540

541 TCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGA 600

601 AGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACAC 660

661 AA 705

000021 " STAFEL60

Figure 2B
Interleukin-22

901 CGACTATATACCTACTTTTAAATCAACTGTTTGAATAGAGGCAGAGCTATTTTATATT 960
961 ATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTTACTTCTTC 1020
1021 TGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAAATTTGTAGCTGGTACACTC 1080
1081 TGGCCTGGGTCTCTGAATTCAGCCTGTCACCGATGGCTGACTGATGAAATGGACACGTCT 1140
1141 CATCTGACCCACTCTTCCTTCCACTGAAGGTCTTCACGGGCCCTCCAGGTGGACCAAAGGG 1200
1201 ATGCACAGCGGGCTCGCATGCCCCAGGGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGG 1260
1261 TTTTAGTCATGAATACATAAACAGTCTCAAACCTCGCACAATTTTTTCCCCCTTTTGAAAG 1320
1321 CCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGGAACCTGACATCTTT 1380
1381 GCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCAGG 1440
1441 CTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCT 1500
1501 GTTCTGCAATTCGCCACGAGAGCTAGGTCTTGATCTTTTCTTTAGATTGAAAGTCTGT 1560
1561 CTCTGAACACAATTATTTGTAAAAGTTAGTAGTCTTTTTTAAATCATTAAAAGAGGCTT 1620
1621 GCTGAAAAAAAAAAAAAAAAAAAA 1642

00802T"STEF260

[illegible][illegible]

	60	70	80	90	100	
39	- - - - -	K N F P R T V M V N L N I - H N R N T N T N P K R S S D Y - - - -	IL-17.aa			
41	- - - - -	K D F L Q N V K V N L K V F N S L G A K V S S R R P S D Y - - - -	mIL-17.aa			
38	- - - - -	S F P R S V M V T L S I - R N W N T S - S K R A S D Y - - - -	vIL-17.aa			
51	S R M K P Y A R M E E Y E R N I E - E M V A Q L R N S S E L A Q R - - - -	C E V - - - -	II20.aa			
2	- - - - -	- - - - -	- - - - -	- - - - -	IL-21.aa	
48	P P - H L L A R G A K W G Q A L P V A L V S S L E A A S H R G R H E R P S A T T Q C P V L - R P E E	II21FL.aa				
5	- - - - -	A R A V L S A F H H T L Q L G P P R E Q A R N A S - C P A G G R P A D	IL-22.aa			
12	- - - Q L Y G R - - - -	L A A G V L S A F H H T L Q L G P P R E Q A R N A S - C P A G G R P A D	II22ext.aa			

Figure 3A

[illegible]

	160										170										180										190										200										
109	H	M	N	S	V	P	I	Q	Q	E	I	L	V	L	R	R	E	P	-	-	-	-	-	-	P	H	C	P	N	S	F	R	L	E	K	I	L	-	-	V	S	V	G	C	T	C	V	T	P	IL-17.aa	
112	H	M	N	S	V	L	I	Q	Q	E	I	L	V	L	K	R	E	P	-	-	-	-	-	-	E	S	C	P	F	T	F	R	V	E	K	M	L	-	-	V	G	V	G	C	T	C	V	A	S	mIL-17.aa	
105	H	M	N	S	V	P	I	Q	Q	E	I	L	V	V	R	K	G	H	-	-	-	-	-	-	Q	P	C	P	N	S	F	R	L	E	K	M	L	-	-	V	T	V	G	C	T	C	V	T	P	vIL-17.aa	
137	S	M	V	S	V	P	V	F	-	S	Q	V	P	V	R	R	R	L	C	P	P	P	R	T	G	P	C	R	Q	-	-	-	-	-	R	A	V	M	E	T	I	A	V	G	C	T	C	I	-	-	IL20.aa
35	A	L	N	S	V	R	L	L	Q	S	L	V	L	R	R	R	P	C	S	R	D	G	S	G	L	P	T	P	G	A	F	A	F	H	T	E	F	I	H	V	P	V	G	C	T	C	V	-	-	IL-21.aa	
145	A	L	N	S	V	R	L	L	Q	S	L	V	L	R	R	R	P	C	S	R	D	G	S	G	L	P	T	P	G	A	F	A	F	H	T	E	F	I	H	V	P	V	G	C	T	C	V	-	-	IL21FL.aa	
88	R	F	R	S	A	P	V	Y	M	P	T	V	L	R	R	T	P	A	C	A	G	G	R	S	V	-	-	-	-	-	-	-	-	Y	T	E	A	Y	V	T	I	P	V	G	C	T	C	P	E	IL-22.aa	
101	R	F	R	S	A	P	V	Y	M	P	T	V	L	R	R	T	P	A	C	A	G	G	R	S	V	-	-	-	-	-	-	-	Y	T	E	A	Y	V	T	I	P	V	G	C	T	C	P	E	IL22ext.aa		

Figure 3B

	210	220	230	
150	± V H H V A			IL-17.aa
153	± V R Q A A			mIL-17.aa
146	± V H N V D			vIL-17.aa
180	- - - - -	- - - - -	- - - - -	IL20.aa
83	- - - - -	- - - - -	- L P R S V	IL-21.aa
193	- - - - -	- - - - -	- L P R S V	IL21FL.aa
131	P E K D A D S I N S S I D K Q G A K L L L G P N D A P A G P			IL-22.aa
44	P E K D A D S I N S S I D K Q G A K L L L G P N D A P A G P			IL22ext.aa

Figure 3C

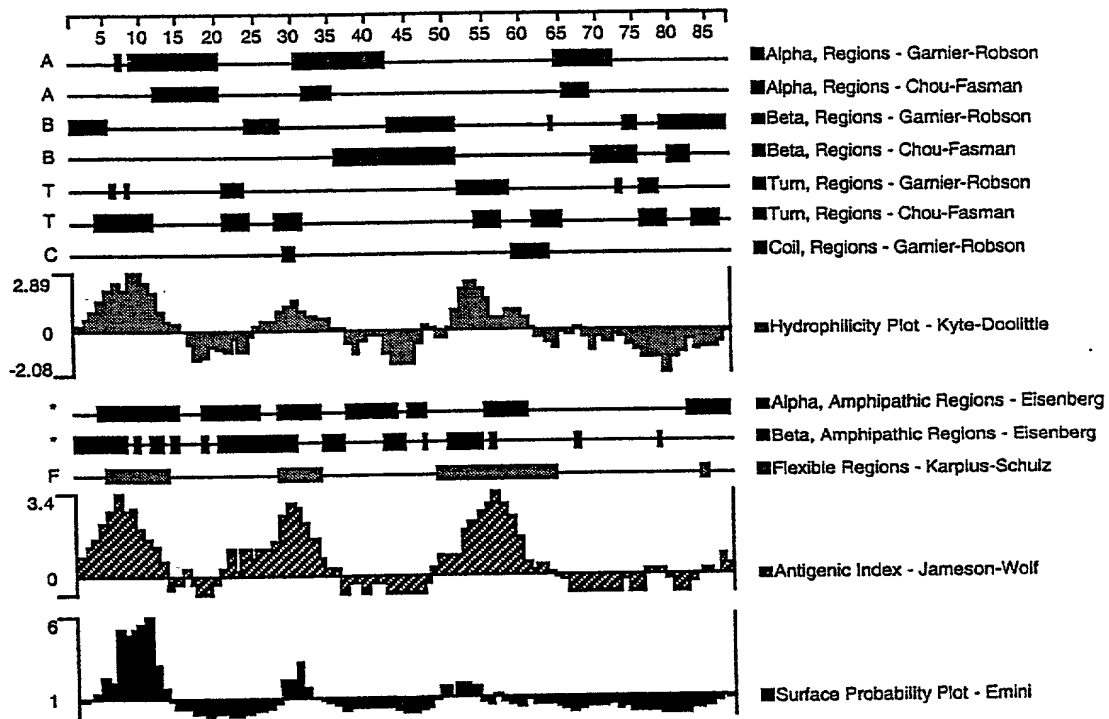
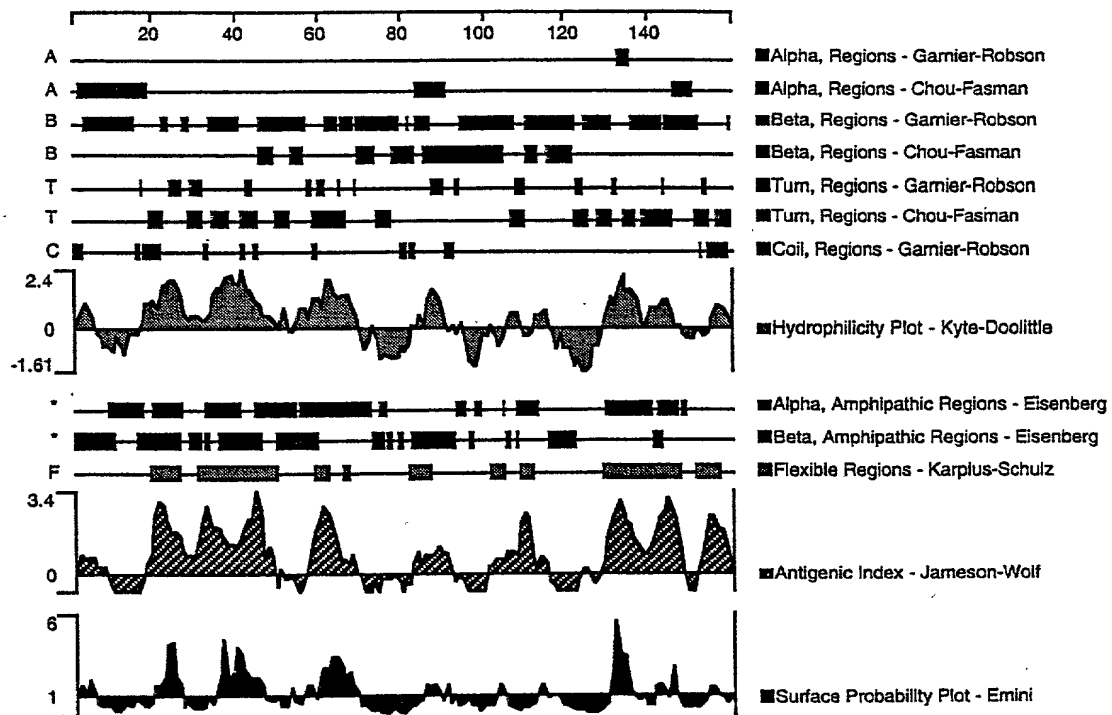


Figure 5
Interleukin-22 Polypeptide Analysis



000001 " 91416200

Figure 6A
Interleukin-21

1 GCTCCAAGCCCAGCCTGCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGTTT 60
1 M T L L P G L L F 9

61 CTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCAC 120
10 L T W L H T C L A H H D P S L R G H P H 29

121 AGTCACGGTACCCCACTGCTACTCGGCTGAGGAAGTCCCCCTGGGCCAGGCCCCCA 180
30 S H G T P H C Y S A E E L P L G Q A P P 49
Domain V

181 CACCTGCTGGCTCGAGGTGCCAAGTGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGC 240
50 H L L A R G A K W G Q A L P V A L V S S 69
Domain VI

241 CTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCCG 300
70 L E A A S H R G R H E R P S A T T Q C P 89

301 GTGCTGCGGCCGAGGAGGTGTGGAGGCAGACACCCACCAGCGCTCCATCTCACCTGG 360
90 V L R P E E V L E A D T H Q R S I S P W 109
Domain VII

361 AGATACCGGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGC 420
110 R Y R V D T D E D R Y P Q K L A F A E C 129
Domain I Domain II

421 CTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGAGACAGCTGCGCTCAACTCCGTG 480
130 L C R G C I D A R T G R E T A A L N S V 149
Domain II

481 CGGCTGCTCCAGAGCCTGCTGGTGTGCTGCGCGCCGGCCCTGCTCCCGCGACGGCTCGGGG 540
150 R L L Q S L L V L R R R P C S R D G S G 169
Domain III

541 CTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCAGTCCCCGTGGGCTGC 600
170 L P T P G A F A F H T E F I H V P V G C 189
Domain IV

601 ACCTGCGTGTGCCCCGTTTCAGTGTGACCGCCAAGGCGGTGGGGCCCTTAGACTGGACAC 660
190 T C V L P R S V 197
Domain IV

661 GTGTGCTCCCCAGAGGGCACCCCTATTATGTGTATTATTGTATTATATGCCTCCC 720

721 CCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTTC 780

09731816 120200

Figure 6B
Interleukin-21

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781 TCCTCATCTCCAGCCTCAGTAGTTGGGGGTWGAAGGAGCTCAGCACCTCTTCCAGCCCTT 840
      . . . . .
841 AAAGCTGCAGAAAAGGTGTACACGGCTGCCTGTACCTTGGYTCCCTGTCCTGCTCCCGG 900
      . . . . .
901 CTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG 960
      . . . . .
961 GAAGTACCCTGTTTCTTAAACAATTATTTAAGTGACGTGTATTATTAAACTGATGAAC 1020
      . . . . .
1021 ACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1067

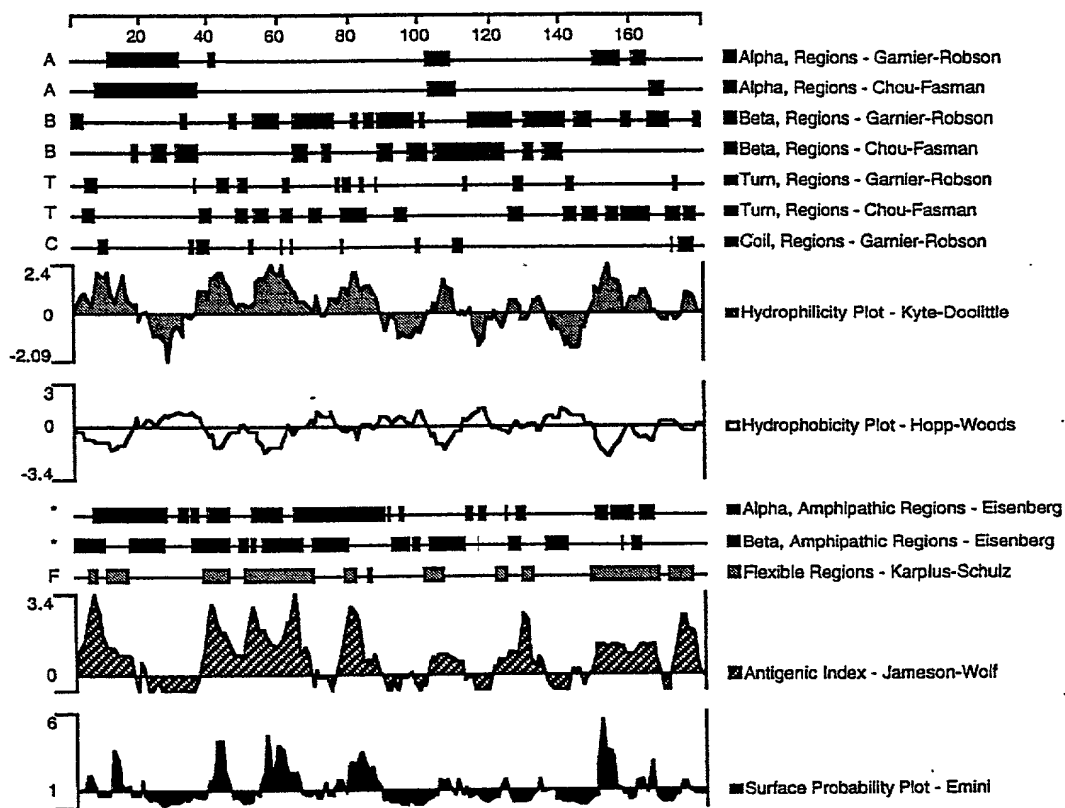
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[illegible]

1	GGCTGCGCGGACCGGCCGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGGGCCGCG	60
1	G C A D R P E E L L E Q L Y G R L <u>A A G</u>	20
	CD-VI	
	#	
61	GTGCTCAGTGCCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCG	120
21	<u>V L S</u> A F H H T L Q L G P R E Q A R N A	40
	CD-VI	
121	AGCTGCCCGGCAGGGGGCAGGCCCGCGACCGCGCTTCCGGCGCGCCACCAACCTGCGC	180
41	S C P A G G R P A D R R F R P P T N L <u>R</u>	60
181	AGCGTGTGCGCCCTGGGGCTACAGAATCTCCTACGACCGGGCGAGGTACCCAGGTACCTG	240
61	<u>S V S P W</u> A Y R <u>I S Y D P A R Y P</u> R Y L	80
	CD-VII	CD-I
241	CCTGAAGCCTACTGCCTGTGCGGGGCTGCCTGACCGGGCTGTTCGGCGAGGAGGACGTG	300
81	P E A Y <u>C L C R G C</u> L T G L F G E E D V	100
	CD-II	
301	CGCTTCCGCAGCGCCCTGTCTACATGCCCCACCGTCTGCTCTGCGCCGCACCCCCGCCTGC	360
101	R F R S A P V Y M P T <u>V V L R R T P</u> A C	120
	CD-III	
361	GCGGCGCGCCGTTCCGTCTACACCGAGGCCTACGTACCATCCCCGTGGGCTGCACCTGC	420
121	A G G R S V Y T E A Y V T <u>I P V G C T C</u>	140
	CD-IV	
	#	
421	GTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCC	480
141	<u>V</u> P E P E K D A D S I N S S I D K Q G A	160
	CD-IV	
481	AAGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCCTGA	522
161	K L L L G P N D A P A G P	174

481 AAGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCCTGA 522
161 K L L L G P N D A P A G P 174

Figure 9
Interleukin-22 Polypeptide Analysis



09734815 120800
008021 9181260